



seqSU0411PCT.txt  
SEQUENCE LISTING

<110> SUNTORY LIMITED

<120> A gene encoding an enzyme catalyzing biosynthesis of lignan,  
and the use thereof

<130> SU0411/PCT

<150> JP 2003-341313

<151> 2003-09-30

<150> JP 2003-432383

<151> 2003-12-26

<160> 79

<170> PatentIn Ver. 2.1

<210> 1

<211> 506

<212> PRT

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<223> SiP189

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## seqSU0411PCT.txt

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 Ile Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu Ile Arg Ser  
 325 330 335  
 Val Val Gly Lys Lys Gly Ser Val Ala Glu Asp Asp Ile Gln Lys Leu  
 340 345 350  
 Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro  
 355 360 365  
 Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp  
 370 375 380  
 Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala  
 385 390 395 400  
 Ile Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro  
 405 410 415  
 Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly  
 420 425 430  
 Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu  
 435 440 445  
 Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe  
 450 455 460

seqSU0411PCT.txt

His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp  
465 470 475 480

Phe Leu Pro Gly Ile Thr Thr His Lys Lys Asn Ala Leu Tyr Leu Met  
485 490 495

Ala Lys Ser Tyr Leu  
500

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<213> Sesamum indicum

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<223> siP288

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cttctgcttc acgtgagccg gattcacgac aattgcacgg agattatggg gaagtcccga 180  
cggggaactt ttcatattccg ggtgccctgg ttggctgata tggacatgat ggggactgct 240  
gatcctgaga atgttcacta cattatgagc gcgaacttcc agaatttccc gaaaggcccc 300  
aagttcaggg aaatttttga tgttcttggg gatgggattt tcaatgcaga ttcggagtcc 360  
tggagggacc agagaagggt tgccagggcc ctgatttctc accatggttt cctccggttt 420  
ctggcgaaga tcagccgtga gaaggtagag aaaggcctga ttccagttct tgaaacggtg 480  
tgcttggaat atcgggtggt cgatttgagc gatttggtcc agaggttgac gtttgataca 540  
acttgtagat ttgttactgg ttatgatcct ggatgcttgt ctgttgattt gcctgatgtt 600  
cctttctcga aagccctaga tgatgccgaa gaagcgatat tcatgcgcca tgtggttcct 660  
gaaaagattt ggaaacttca gaggtgggtt ggggttggtat ctgagagaaa attgagcaag 720  
gctcgtgaag tcttgtagat cgtcattggc aggtatatcg cgctgaagcg cggcgaaatg 780  
agaagccgag gaatttcgat tgattgtgaa aatgaagatg gtgtggatct gctcacgtct 840  
tacctgactg tgggagacga tggtagtcaa acccatgatt tgaaatgtga tgacaagttc 900  
ttgagggaca cgatactgaa tctaattgatt gcaggcgagg acacgacgag ttctgctctg 960  
acatgggtta tatggcttgt gtcgacacat gctgaagtgg aaaagaggat cagggatgaa 1020  
ctgaagtcct ttctgccccg cggagaacgt gaaaagtggc gtgtgttttg ggttgaagaa 1080  
accaagaagt tggtttacat gcatggagca atttgcgaag ccctacgact atatccacca 1140  
gtccccgttc agcataagga gccggtggaa ccagatatcc ttccgagcgg gcattttgtg 1200  
gaaccgacaa tgaaagtgat gttctcattg tacgccatgg gacggatgga atccgttttg 1260  
ggcgaggatt gcttggaatt caagccggag aggtggattt ctgatagggg atcgatcaag 1320  
cacgagccct catacaagtt cttggctttc aatgctggtc cgaggacttg cttgggggaa 1380  
gatgtggctt tcgctcaggt gaaggcagtg gccgccacct taatccataa ctaccaagtt 1440  
cacgtggcag acggccaccg cgtgctgccc aattgttcca tcatcctcta catgaggaat 1500  
ggattgaagg ttagggttgc caatagatgg tctgctaaga aaaat 1545

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<212> PRT  
<213> Sesamum indicum

<220>  
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<400> 56  
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Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp  
20 25 30

Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile  
Page 16



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35                               40                               45
His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe
  50                               55                               60
His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Met Gly Thr Ala
  65                               70                               75                               80
Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe
  85                               90                               95
Pro Lys Gly Pro Lys Phe Arg Glu Ile Phe Asp Val Leu Gly Asp Gly
 100                               105                               110
Ile Phe Asn Ala Asp Ser Glu Ser Trp Arg Asp Gln Arg Arg Val Ala
 115                               120                               125
Arg Ala Leu Ile Ser His His Gly Phe Leu Arg Phe Leu Ala Lys Ile
 130                               135                               140
Ser Arg Glu Lys Val Glu Lys Gly Leu Ile Pro Val Leu Glu Thr Val
 145                               150                               155                               160
Cys Leu Glu Asn Arg Val Val Asp Leu Gln Asp Leu Phe Gln Arg Leu
 165                               170                               175
Thr Phe Asp Thr Thr Cys Thr Phe Val Thr Gly Tyr Asp Pro Gly Cys
 180                               185                               190
Leu Ser Val Asp Leu Pro Asp Val Pro Phe Ser Lys Ala Leu Asp Asp
 195                               200                               205
Ala Glu Glu Ala Ile Phe Met Arg His Val Val Pro Glu Lys Ile Trp
 210                               215                               220
Lys Leu Gln Arg Trp Phe Gly Val Gly Ser Glu Arg Lys Leu Ser Lys
 225                               230                               235                               240
Ala Arg Glu Val Leu Asp Ser Val Ile Gly Arg Tyr Ile Ala Leu Lys
 245                               250                               255
Arg Gly Glu Met Arg Ser Arg Gly Ile Ser Ile Asp Cys Glu Asn Glu
 260                               265                               270
Asp Gly Val Asp Leu Leu Thr Ser Tyr Met Thr Val Gly Asp Asp Gly
 275                               280                               285
Thr Gln Thr His Asp Leu Lys Cys Asp Asp Lys Phe Leu Arg Asp Thr
 290                               295                               300
Ile Leu Asn Leu Met Ile Ala Gly Arg Asp Thr Thr Ser Ser Ala Leu
 305                               310                               315
Thr Trp Phe Ile Trp Leu Val Ser Thr His Ala Glu Val Glu Lys Arg
 325                               330                               335
Ile Arg Asp Glu Leu Lys Ser Phe Leu Pro Ala Gly Glu Arg Glu Lys
 340                               345                               350
Trp Arg Val Phe Gly Val Glu Glu Thr Lys Lys Leu Val Tyr Met His
 355                               360                               365
Gly Ala Ile Cys Glu Ala Leu Arg Leu Tyr Pro Pro Val Pro Phe Gln

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## seqSU0411PCT.txt

370

375

380

His Lys Glu Pro Val Glu Pro Asp Ile Leu Pro Ser Gly His Phe Val  
 385 390 395 400

Glu Pro Thr Met Lys Val Met Phe Ser Leu Tyr Ala Met Gly Arg Met  
 405 410 415

Glu Ser Val Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp  
 420 425 430

Ile Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu  
 435 440 445

Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe  
 450 455 460

Ala Gln Val Lys Ala Val Ala Ala Thr Leu Ile His Asn Tyr Gln Val  
 465 470 475 480

His Val Ala Asp Gly His Arg Val Leu Pro Asn Cys Ser Ile Ile Leu  
 485 490 495

Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala  
 500 505 510

Lys Lys Asn  
 515

<210> 57  
 <211> 1494  
 <212> DNA  
 <213> Sesamum indicum

<220>  
 <223> SiP168

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 aaacctcttc ccataatcgg caacattctt gagcttggtg agaaacccca ccaatctctc 180  
 gccaaactct ccaaaacctt cgggccccctg atgcgtctca agctgggaac catgacaaca 240  
 gttgttgat cctccccgga aatctccagg atcgtgctgc aacaatatga ccaagttttc 300  
 tccagccgaa cacacgcaga tgccatccga gcacttgacc accacaaaca ttccgtcgcc 360  
 tggataccgg cggacaatca gtggcgga aaatccgtaa atccgtaaac tgtgcaaaga gaagatgttt 420  
 tcgggccaaa agcttgatgc gaaccagggc ctgaggaggg agaagttgct taatttgcaa 480  
 gactatgtga atgaatgctg cgttagtggc caggctcgtg atattggtgt agctgccttt 540  
 acgacgacct ttaatctgat atcggccact cttttctcgg tggattttgc tgattttggt 600  
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 ccaaattttg ctgattgttt cctctttctt cggctggttg atccacaggg catcttccgc 720  
 cagaccacgt tacatttcaa caagtgtttt aagatctttg atgaaattat ccgtcaaagg 780  
 ctacagacca atgattcggg gacgaaaagt gacatgctga aagagcttct tgaatcaaac 840  
 cagaaagatg agtctgaatt gagctttgac gagatcaagc atttactcct ggatctactt 900  
 gtcgcaggaa cggacacaac ttcagttaca gtggaatggg caatgacgga gctagtgcgc 960  
 caccctgaga aaatgtcgaa agccagaaat gagttaagaa atgtggtggg actgaataaa 1020  
 gaaattcaag aatcagacat ctcaagactc ccttacctac gagcagtggg gaaagaaagt 1080  
 ttcaggcttc accctgcaac tcctttatcg gtacctcaca aggccgacga ggaagcagaa 1140  
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1494

&lt;210&gt; 58

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Sesamum indicum

&lt;220&gt;

&lt;223&gt; siP168

&lt;400&gt; 58

Met Asp Leu Leu Leu Ser Leu Val Leu Leu Leu Cys Ser Ala Ala Cys  
1 5 10 15Ile Trp Phe Leu Arg Val Val Leu Lys Pro Asn Pro Gly Pro Arg Lys  
20 25 30Ser Ala Asn Leu Pro Pro Gly Pro Lys Pro Leu Pro Ile Ile Gly Asn  
35 40 45Ile Leu Glu Leu Gly Glu Lys Pro His Gln Ser Leu Ala Lys Leu Ser  
50 55 60Lys Thr Tyr Gly Pro Leu Met Arg Leu Lys Leu Gly Thr Met Thr Thr  
65 70 75 80Val Val Val Ser Ser Pro Glu Ile Ser Arg Ile Val Leu Gln Gln Tyr  
85 90 95Asp Gln Val Phe Ser Ser Arg Thr His Ala Asp Ala Ile Arg Ala Leu  
100 105 110Asp His His Lys His Ser Val Ala Trp Ile Pro Ala Asp Asn Gln Trp  
115 120 125Arg Lys Ile Arg Lys Leu Cys Lys Glu Lys Met Phe Ser Gly Gln Lys  
130 135 140Leu Asp Ala Asn Gln Gly Leu Arg Arg Glu Lys Leu Arg Asn Leu Gln  
145 150 155 160Asp Tyr Val Asn Glu Cys Cys Val Ser Gly Gln Val Val Asp Ile Gly  
165 170 175Val Ala Ala Phe Thr Thr Thr Leu Asn Leu Ile Ser Ala Thr Leu Phe  
180 185 190Ser Val Asp Phe Ala Asp Phe Gly Ser Gly Ser Ser Gln Glu Leu Lys  
195 200 205Asp Val Met Ser Gly Ile Ala Ser Ile Ile Gly Arg Pro Asn Phe Ala  
210 215 220Asp Cys Phe Pro Leu Leu Arg Leu Val Asp Pro Gln Gly Ile Phe Arg  
225 230 235 240Gln Thr Thr Leu His Phe Asn Lys Cys Phe Lys Ile Phe Asp Glu Ile  
245 250 255Ile Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met  
260 265 270

## seqSU0411PCT.txt

Leu Lys Glu Leu Leu Glu Ile Asn Gln Lys Asp Glu Ser Glu Leu Ser  
 275 280 285  
 Phe Asp Glu Ile Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr  
 290 295 300  
 Asp Thr Thr Ser Val Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg  
 305 310 315 320  
 His Pro Glu Lys Met Ser Lys Ala Arg Asn Glu Leu Arg Asn Val Val  
 325 330 335  
 Gly Leu Asn Lys Glu Ile Gln Glu Ser Asp Ile Ser Arg Leu Pro Tyr  
 340 345 350  
 Leu Arg Ala Val Val Lys Glu Ser Phe Arg Leu His Pro Ala Thr Pro  
 355 360 365  
 Leu Ser Val Pro His Lys Ala Asp Glu Glu Ala Glu Ile Asn Gly Tyr  
 370 375 380  
 Ile Val Pro Lys Gly Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly  
 385 390 395 400  
 Arg Asp Ser Ser Ile Trp Arg Asn Pro Asp Val Phe Met Pro Glu Arg  
 405 410 415  
 Phe Leu Glu Thr Glu Ile Asp Val Arg Gly Gln His Phe Glu Leu Leu  
 420 425 430  
 Pro Phe Gly Gly Gly Arg Arg Ile Cys Val Gly Leu Pro Leu Ala Tyr  
 435 440 445  
 Arg Met Ile His Leu Val Leu Ala Thr Phe Ile Ser Asp Tyr Asp Trp  
 450 455 460  
 Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys  
 465 470 475 480  
 Phe Gly Leu Thr Leu Gln Lys Ala Ile Pro Leu Lys Ala Leu Pro Val  
 485 490 495

Lys Ile

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 <211> 1545  
 <212> DNA  
 <213> Sesamum indicum

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 aggtaccatc ccattggtgg taccgtgttc aaccagctgc tgaacttcta taggttgc 180  
 gattatatgg ctgatcttgc aggaagtac aagacttaca gactgattgc cccttttcg 240  
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 agttatggca agggacctta caattgcagc attctggggg atttgtttgg tgaaggaatt 360  
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aaatcaactt	ttgattctat	ttcggaagtt	gctttaggag	ttgagcttga	cagcttgagg	600
ggttcaaattg	aagaagggtgc	caaatttagc	attgctgcag	acgacgtgag	tatgaggaca	660
ctttggagat	acgtggatgt	tctgtggaag	ttaaagagag	ctctaaatgt	tggttcagaa	720
gcaaaactga	agaaaagcct	tcaagtggtt	gatgaatttg	tgtataagct	gattcatagt	780
aggactcagc	aaatgaacat	gccaggaaat	gattctgtta	tcgacgtgaa	gaaagacgac	840
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ataagcttta	tagttgctgg	taaagacaca	acagcaacaa	ctctctcctg	gtttattttac	960
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ggctgcaaag	aggtagcaga	tatctcagaa	ttttcagcct	tggtgacaga	agaagctttg	1080
ggcaagatgc	attatctcca	tgcagcattg	acagaaacac	ttaggatttta	tccagcagtt	1140
gcggtggatg	caaagcaatg	tttgtgtgat	gatataatgc	cggatggggt	cagtgttaag	1200
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gccagccctt	ttaagtttac	agctttccag	gccggccctc	gtctttgttt	ggggaaagag	1380
tttgcttatc	ggcagatgaa	gatatttcca	gccattctgc	tgagattctt	taccatgaaa	1440
ctaagtcatg	aaagaaagac	agtaacttac	agaccaatgc	ctactcttct	catcgacggt	1500
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<210> 60
<211> 515
<212> PRT
<213> Sesamum indicum
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<220>  
<223> sip236

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      20      25      30
Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr
      35      40      45
Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala
      50      55      60
Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg
      65      70      75      80
Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys
      85      90      95
Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu
      100      105      110
Gly Asp Leu Phe Gly Glu Gly Ile Phe Ala Ile Asp Gly His Lys Trp
      115      120      125
Arg Glu Gln Arg Lys Val Ser Ser Leu Glu Phe Ser Thr Arg Val Leu
      130      135      140
Arg Asp Tyr Ser Ser Ile Val Phe Arg Lys Asn Ala Val Arg Leu Ala
      145      150      155      160
Lys Ile Leu Ser Gly Ala Ala Thr Ser Asn Gln Pro Val Asp Ile Gln
      165      170      175
Asp Leu Phe Met Lys Ser Thr Phe Asp Ser Ile Ser Glu Val Ala Leu

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## seqSU0411PCT.txt

180										185					190				
Gly	Val	Glu	Leu	Asp	Ser	Leu	Gly	Gly	Ser	Asn	Glu	Glu	Gly	Ala	Lys				
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Phe	Ser	Ile	Ala	Ala	Asp	Asp	Val	Ser	Met	Arg	Thr	Leu	Trp	Arg	Tyr				
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Val	Asp	Val	Leu	Trp	Lys	Leu	Lys	Arg	Ala	Leu	Asn	Val	Gly	Ser	Glu				
	225				230					235					240				
Ala	Lys	Leu	Lys	Lys	Ser	Leu	Gln	Val	Val	Asp	Glu	Phe	Val	Tyr	Lys				
				245					250					255					
Leu	Ile	His	Ser	Arg	Thr	Gln	Gln	Met	Asn	Met	Pro	Gly	Asn	Asp	Ser				
			260					265					270						
Val	Met	Gln	Leu	Lys	Lys	Asp	Asp	Ile	Leu	Ser	Arg	Phe	Leu	Gln	Leu				
		275					280					285							
Thr	Glu	Ala	Thr	Pro	Lys	Tyr	Leu	Arg	Asp	Ile	Thr	Ile	Ser	Phe	Ile				
	290					295					300								
Val	Ala	Gly	Lys	Asp	Thr	Thr	Ala	Thr	Thr	Leu	Ser	Trp	Phe	Ile	Tyr				
	305				310					315					320				
Met	Leu	Cys	Lys	Tyr	Pro	His	Val	Gln	Glu	Lys	Val	Glu	Gln	Glu	Ile				
				325					330					335					
Lys	Asp	Ala	Thr	Gly	Cys	Lys	Glu	Val	Ala	Asp	Ile	Ser	Glu	Phe	Ser				
			340					345					350						
Ala	Cys	Val	Thr	Glu	Glu	Ala	Leu	Gly	Lys	Met	His	Tyr	Leu	His	Ala				
		355					360					365							
Ala	Leu	Thr	Glu	Thr	Leu	Arg	Ile	Tyr	Pro	Ala	Val	Ala	Val	Asp	Ala				
	370					375					380								
Lys	Gln	Cys	Leu	Cys	Asp	Asp	Ile	Met	Pro	Asp	Gly	Phe	Ser	Val	Lys				
	385				390					395					400				
Lys	Gly	Asp	Met	Val	Ala	Tyr	Gln	Pro	Tyr	Ala	Met	Gly	Arg	Met	Lys				
				405					410					415					
Ser	Ile	Trp	Gly	Asn	Asp	Ala	Glu	Glu	Phe	Lys	Pro	Glu	Arg	Trp	Leu				
			420					425					430						
Asp	Lys	Asn	Gly	Cys	Phe	Gln	Gln	Ala	Ser	Pro	Phe	Lys	Phe	Thr	Ala				
		435					440					445							
Phe	Gln	Ala	Gly	Pro	Arg	Leu	Cys	Leu	Gly	Lys	Glu	Phe	Ala	Tyr	Arg				
	450					455					460								
Gln	Met	Lys	Ile	Phe	Ser	Ala	Ile	Leu	Leu	Arg	Phe	Phe	Thr	Met	Lys				
	465				470					475					480				
Leu	Ser	Asp	Glu	Arg	Lys	Thr	Val	Asn	Tyr	Arg	Pro	Met	Leu	Thr	Leu				
				485					490					495					
Leu	Ile	Asp	Gly	Gly	Leu	Ile	Val	Arg	Pro	Phe	His	Arg	Met	Asp	Glu				
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Lys	Thr	Ala																	

515

<210> 61  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, Bam-SST-FW2

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34

<210> 62  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, SiP189-Nco-RV

<400> 62  
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24

<210> 63  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, GR-SST-RV1

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27

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 <211> 506  
 <212> PRT  
 <213> Sesamum radiatum

<220>  
 <223> SrSiP189

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 Ile Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His  
 35 40 45

## seqSU0411PCT.txt

Val His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser  
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 Gln Lys Leu Gly Pro Ile Phe Ser Leu Arg Phe Gly Thr Arg Leu Val  
 65 70 75 80  
 Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr  
 85 90 95  
 Asp Ile Val Leu Ala Asn Arg Pro Gln Pro Ser Val Asp Arg Arg Ser  
 100 105 110  
 Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His  
 115 120 125  
 Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr  
 130 135 140  
 Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met  
 145 150 155 160  
 Ile Ser Ser Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn  
 165 170 175  
 Leu Glu Thr Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met  
 180 185 190  
 Val Ala Gly Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu  
 195 200 205  
 Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser  
 210 215 220  
 Ala Ser Asn Pro Gly Glu Ile Phe Pro Ile Leu Arg Trp Leu Gly Phe  
 225 230 235 240  
 Asn Gly Leu Glu Lys Lys Leu Ala Val His Ala Arg Lys Thr Asp Glu  
 245 250 255  
 Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn  
 260 265 270  
 Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln Pro Glu Tyr  
 275 280 285  
 Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala  
 290 295 300  
 Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Ile  
 305 310 315 320  
 Leu Asn His Pro Gln Val Leu Glu Lys Ala Arg Lys Glu Leu Asp Thr  
 325 330 335  
 Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu  
 340 345 350  
 Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser  
 355 360 365  
 Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly  
 370 375 380



seqSU0411PCT.txt

Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Leu Val Asn Ala Trp Ala  
 385 390 395 400  
 Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro  
 405 410 415  
 Asp Arg Phe Glu Thr Met Glu Val Glu Thr His Lys Leu Leu Pro Phe  
 420 425 430  
 Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe  
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 Val Gly Leu Ala Leu Gly Ser Leu Ile Gln Cys Phe Glu Trp Glu Arg  
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 <213> Sesamum radiatum

<220>  
 <223> srSiP189

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<210> 66  
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 <213> Artificial Sequence

<220>  
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 Synthesized Primer Sequence, NtUBQ-FW

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<210> 67  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, NtUBQ-RW

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<210> 68  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, SiP189-bam-FW

<400> 68  
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<210> 69  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, SiP189-nco-RV

<400> 69  
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<210> 70  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, STAR-LF1

<400> 70

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25

&lt;210&gt; 71

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
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25

&lt;210&gt; 72

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
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24

&lt;210&gt; 73

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
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24

&lt;210&gt; 74

&lt;211&gt; 3069

&lt;212&gt; DNA

&lt;213&gt; Sesamun indium

&lt;400&gt; 74

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<210> 75  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, gSST-FW1

<400> 75  
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<210> 76  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, gSST-RV2

<400> 76  
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<210> 77  
 <211> 2815  
 <212> DNA  
 <213> Sesamum radiatum  
 <220>  
 <221> misc\_feature  
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 <223> n stands for any base

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<210> 78

&lt;211&gt; 507

&lt;212&gt; PRT

&lt;213&gt; Sesumum alatum

&lt;400&gt; 78

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 35 40 45  
 Leu His Leu Ile Lys Asn Pro Leu His Arg Thr Leu Tyr Asp Cys Ser  
 50 55 60  
 Gln Lys Leu Gly Ser Ile Phe Ser Val Trp Phe Gly Ser Arg Leu Val  
 65 70 75 80  
 Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr  
 85 90 95  
 Asp Ile Val Leu Ala Asn Arg Pro Asp Leu His Leu Asp Leu Arg Ser  
 100 105 110  
 Leu Gly Ala Ser Thr Ile Ser Val Ile Gly Ala Pro Tyr Gly Asp His  
 115 120 125  
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 Arg Leu Ala Ser Phe Leu Ser Ile Arg Arg Asp Glu Arg Asp Arg Met  
 145 150 155 160  
 Ile Ser Gly Leu Tyr Lys Ile Ser Ser Ala Gly Leu Ala Lys Val Asn  
 165 170 175  
 Leu Glu Ala Lys Ile Ala Glu Leu Thr Phe Asn Asn Leu Met Arg Met  
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 Ala Lys Arg Phe Arg Asp Met Thr Lys Glu Ala Leu Glu Leu Met Asn  
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 225 230 235 240  
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 260 265 270  
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 275 280 285  
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 Arg Tyr Leu His Tyr Ile Ile Leu Glu Thr Leu Arg Leu Phe Pro Ser  
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 Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Ile Val Asn Ala Trp Ala  
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&lt;210&gt; 79

&lt;211&gt; 1524

&lt;212&gt; DNA

&lt;213&gt; Sesumum alatum

&lt;400&gt; 79

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